

Identification of Bifid Bacterium Animals Ssp. Lactic from Egyptian Women Breast Milk and Feces of Breast Fed Infant Based on Molecular Level

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Bifid bacterium represent one of the major genera of the intestinal tract of human and animals used as probiotics in dairy and nondairy foods for restore the intestinal micro flora which confers a health benefit. The identification of bifid bacterium by phenotypic features is commonly unreliable, time, money, and effort consuming. We sought to improve the Bifid bacterium identification method based on molecular level to identify probiotic bacteria in complex microbial communities. The application of 16S-23S rRNA Oligonucleotides primers is the best and most reliable, rapid, and precise species and sub species identification approach. The ribosomal antigenic spacer region (ISR) located between the highly conserved 16S rRNA and 23S rRNA shows a high degree of variation in length and sequence and potential for intra species discrimination and providing the phylogenetic Relationship of the Genus Bifid bacterium spp. Results showed that one of the two primer sets Bflac2-Bflac5 species specific gives positive results differentiating between *B. animalis* ssp. Lactic isolated from breast fed infants milk of human and that isolated from feces of breast fed infant and detecting reference strain for *B. animalis* ssp. Lactic DSM10140. DNA sequences of the two strains were submitted to the Genbank NCBI under accession number (KT758845) named as *B. animalis* ssp. Lactic Egm1 (Egyptian milk) and accession number (KT758846) named as Egm1 Egyptian feces while the second primer give false positive result. Also, we aim to obtain patent protection under Intellectual property rights (IPRs) for *B. animalis* ssp. Lact which was isolated from Egyptian resources to be used for a better and healthier food and dairy products.